

SEQUENCE LISTING

<110> University of Saskatchewan Technologies Inc.

<120> PLANT STRESS TOLERANCE GENES, AND USES THEREFOR

<130> 47968-PT

<150> US 60/426,012

<151> 2002-10-14

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1420

<212> DNA

<213> Bromus

<220>

<221> misc feature

<222> (1212)..(1212)

<223> n = a, c, g, or t

<220>

<221> CDS

<222> (77)..(1231)

<223>

<400> 1

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gtcgcaatcc attcagagca cgcaaagcac gcgagcagct gcgatttcta gattctagct      60
cgggacgatac agatca atg gcg gtc atg tcg cgg tcc agg agg ctg gcg gcg      112
                Met Ala Val Met Ser Arg Ser Arg Arg Leu Ala Ala
                1                5                10

ccc gcg ctg ctg gtg ctg cta gcg ctg gcg gcc gtg gcc gtg gcg gag      160
Pro Ala Leu Leu Val Leu Leu Ala Leu Ala Ala Val Ala Val Ala Glu
                15                20                25

acg acg ctg gac ggc gcg gag gtg gcg ccg ggc aag gag gag tcg tcg      208
Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu Ser Ser
                30                35                40

tgg gcg ggg tgg gcc aag gac aag gtc tcg gaa ggc ctc ggc ctg gac      256
Trp Ala Gly Trp Ala Lys Asp Lys Val Ser Glu Gly Leu Gly Leu Asp
                45                50                55                60

aag atc tcc gag ggg ctc ggg ctc aag cac cac gcc gac gag gag gag      304
Lys Ile Ser Glu Gly Leu Gly Leu Lys His His Ala Asp Glu Glu Glu
                65                70                75

gcc gcg cgc aag gcc gga cac acc gtc aag tcc gcc cgc gag acc gcc      352
Ala Ala Arg Lys Ala Gly His Thr Val Lys Ser Ala Arg Glu Thr Ala
                80                85                90

cag cac gcc gcc tcc gag acg ggg agg cag gcg agc ggc aag gtg ggg      400
Gln His Ala Ala Ser Glu Thr Gly Arg Gln Ala Ser Gly Lys Val Gly
                95                100                105

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gac gcc aag gag gcc gcg gag cag gcg gcg acc ggg gcg gcc aac aag Asp Ala Lys Glu Ala Ala Glu Gln Ala Ala Thr Gly Ala Ala Asn Lys 110 115 120	448
gcg ggg cag gcc aaa gac aag gcg gcg gag acg gtg aag ggc acg gcc Ala Gly Gln Ala Lys Asp Lys Ala Ala Glu Thr Val Lys Gly Thr Ala 125 130 135 140	496
ggc gag gcg tcc aag aag gcg gag cag gcc aag cac aag acc aag gag Gly Glu Ala Ser Lys Lys Ala Glu Gln Ala Lys His Lys Thr Lys Glu 145 150 155	544
gcc gcg gag gcg gcc gcc aag acg ggc gcc gag acg cac gag cgg tcg Ala Ala Glu Ala Ala Ala Lys Thr Gly Ala Glu Thr His Glu Arg Ser 160 165 170	592
aag cag ggc aag gcc aag gtg gag gag atg gcc agg gag tgg tac gag Lys Gln Gly Lys Ala Lys Val Glu Glu Met Ala Arg Glu Trp Tyr Glu 175 180 185	640
aga gcc aag cac acg gcc ggg gag ggg tac gag acg ctg aag caa acc Arg Ala Lys His Thr Ala Gly Glu Gly Tyr Glu Thr Leu Lys Gln Thr 190 195 200	688
aag gac gcg gct gcg gag aag gca gcg gca gcc aag gac gcc gcc acg Lys Asp Ala Ala Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Thr 205 210 215 220	736
aac aag gcc ggt gcc gcc acg cag acg gcc gcg gag aag gca gcg gca Asn Lys Ala Gly Ala Ala Thr Gln Thr Ala Ala Glu Lys Ala Ala Ala 225 230 235	784
gcc aag gac acc gcc gcc ggt aag gcc aag gct gcg aag gac gct gcg Ala Lys Asp Thr Ala Ala Gly Lys Ala Lys Ala Ala Lys Asp Ala Ala 240 245 250	832
tgg gag gag aca ggc tct gcc aag gac gcc aca tgg cag gcg cag gag Trp Glu Glu Thr Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu 255 260 265	880
aag ctg aag caa tac aac gac gcc gct tcg gag aag gcc gcg gca gcc Lys Leu Lys Gln Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala Ala 270 275 280	928
aag gac gcc gac gct gag aag gcc gcg gca gcc aag gac gcg gcg tgg Lys Asp Ala Asp Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Trp 285 290 295 300	976
aag aac gcc gag gcg gcc aag gga acg gtc gga gag aag gca ggg gcg Lys Asn Ala Glu Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala 305 310 315	1024
gcc aag gac gcc acg ttg gag aag acc gag tcc gcg aag gac gcc gct Ala Lys Asp Ala Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala 320 325 330	1072
tgg gag acg gcg gag gcg gcc aag ggc aag gct aac gag ggg tac gag Trp Glu Thr Ala Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu 335 340 345	1120

aag gtg aag gag aag gac gcg acc aag gaa aag ctc ggc gag gtg aag 1168
 Lys Val Lys Glu Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys
 350 355 360

gac aag gtc acc ggc gca gca tcc gac ggc aag gcg aag aag cnc cgc 1216
 Asp Lys Val Thr Gly Ala Ala Ser Asp Gly Lys Ala Lys Lys Xaa Arg
 365 370 375 380

aat ggc gac gag ctg tgaatgaaca cgatccatcc gcatttcttg ccatagttcc 1271
 Asn Gly Asp Glu Leu
 385

ttcttccatg aatgttttca gtgttcttcg agctagtttt ttttatgttg ttccttttgt 1331
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1420

<210> 2
 <211> 385
 <212> PRT
 <213> Bromus

<220>
 <221> misc feature
 <222> (379)..(379)
 <223> The 'Xaa' at location 379 stands for His, Arg, Pro, or Leu.

<400> 2
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 Val Leu Leu Ala Leu Ala Ala Val Ala Val Ala Glu Thr Thr Leu Asp
 20 25 30
 Gly Ala Glu Val Ala Pro Gly Lys Glu Glu Ser Ser Trp Ala Gly Trp
 35 40 45
 Ala Lys Asp Lys Val Ser Glu Gly Leu Gly Leu Asp Lys Ile Ser Glu
 50 55 60
 Gly Leu Gly Leu Lys His His Ala Asp Glu Glu Glu Ala Ala Arg Lys
 65 70 75 80
 Ala Gly His Thr Val Lys Ser Ala Arg Glu Thr Ala Gln His Ala Ala
 85 90 95
 Ser Glu Thr Gly Arg Gln Ala Ser Gly Lys Val Gly Asp Ala Lys Glu
 100 105 110
 Ala Ala Glu Gln Ala Ala Thr Gly Ala Ala Asn Lys Ala Gly Gln Ala
 115 120 125
 Lys Asp Lys Ala Ala Glu Thr Val Lys Gly Thr Ala Gly Glu Ala Ser
 130 135 140
 Lys Lys Ala Glu Gln Ala Lys His Lys Thr Lys Glu Ala Ala Glu Ala
 145 150 155 160
 Ala Ala Lys Thr Gly Ala Glu Thr His Glu Arg Ser Lys Gln Gly Lys
 165 170 175

Ala Lys Val Glu Glu Met Ala Arg Glu Trp Tyr Glu Arg Ala Lys His
 180 185 190

Thr Ala Gly Glu Gly Tyr Glu Thr Leu Lys Gln Thr Lys Asp Ala Ala
 195 200 205

Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Thr Asn Lys Ala Gly
 210 215 220

Ala Ala Thr Gln Thr Ala Ala Glu Lys Ala Ala Ala Ala Lys Asp Thr
 225 230 235 240

Ala Ala Gly Lys Ala Lys Ala Ala Lys Asp Ala Ala Trp Glu Glu Thr
 245 250 255

Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu Lys Leu Lys Gln
 260 265 270

Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala Ala Lys Asp Ala Asp
 275 280 285

Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Trp Lys Asn Ala Glu
 290 295 300

Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala Ala Lys Asp Ala
 305 310 315 320

Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala Trp Glu Thr Ala
 325 330 335

Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu Lys Val Lys Glu
 340 345 350

Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys Asp Lys Val Thr
 355 360 365

Gly Ala Ala Ser Asp Gly Lys Ala Lys Lys Xaa Arg Asn Gly Asp Glu
 370 375 380

Leu
 385

<210> 3
 <211> 15
 <212> PRT
 <213> Bromus

<400> 3
 Glu Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu
 1 5 10 15

<210> 4
 <211> 6
 <212> PRT
 <213> Bromus

<400> 4
 Lys Ala Ala Ala Ala Lys
 1 5